



# SEQUENCE LISTING

<110> Palese, Peter  
O'Neill, Robert

<120> IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS  
THAT INHIBIT INTERACTION OF HOST CELL PROTEINS  
AND VIRAL PROTEINS REQUIRED FOR VIRAL REPLICATION

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<141> 2003-11-24

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Val Arg Leu Leu His His Asp Asp Pro Glu Val Leu Ala Asp Thr Cys	
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Trp Ala Ile Ser Tyr Leu Thr Asp Gly Pro Asn Glu Arg Ile Gly Met	
245 250 255	
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Val Val Lys Thr Gly Val Val Pro Gln Leu Val Lys Leu Leu Gly Ala	
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Ser Glu Leu Pro Ile Val Thr Pro Ala Leu Arg Ala Ile Gly Asn Ile	
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Val Thr Gly Thr Asp Glu Gln Thr Gln Val Val Ile Asp Ala Gly Ala	
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Leu Ala Val Phe Pro Ser Leu Leu Thr Asn Pro Lys Thr Asn Ile Gln	
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Val Thr Asn Tyr Thr Ser Gly Gly Thr Val Glu Gln Ile Val Tyr Leu	
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Val His Cys Gly Ile Ile Glu Pro Leu Met Asn Leu Leu Thr Ala Lys	
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Asp Thr Lys Ile Ile Leu Val Ile Leu Asp Ala Ile Ser Asn Ile Phe	
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Gln Ala Ala Glu Lys Leu Gly Glu Thr Ser Cys Pro Ser Ser Gln Ile	
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Gln Glu Gln Gly Lys Arg Gln Tyr Arg Asn Glu Ala Ser Glu Ala Ser	
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Gln Asn Arg Glu Thr *	
450	

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Gln Glu Asn Arg Asn Asn Gln Gly Thr Val Asn Trp Ser Val Asp Asp
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Ile Val Lys Gly Ile Asn Ser Ser Asn Val Glu Asn Gln Leu Gln Ala
50     55     60
Thr Gln Ala Ala Arg Lys Leu Leu Ser Arg Glu Lys Gln Pro Pro Ile
65     70     75     80
Asp Asn Ile Ile Arg Ala Gly Leu Ile Pro Lys Phe Val Ser Phe Leu
85     90     95
Gly Arg Thr Asp Cys Ser Pro Ile Gln Phe Glu Ser Ala Trp Ala Leu
100    105    110
Thr Asn Ile Ala Ser Gly Thr Ser Glu Gln Thr Lys Ala Val Val Asp
115    120    125
Gly Gly Ala Ile Pro Ala Phe Ile Ser Leu Leu Ala Ser Pro His Ala
130    135    140
His Ile Ser Glu Gln Ala Val Trp Ala Leu Gly Asn Ile Ala Gly Asp
145    150    155    160
Gly Ser Val Phe Arg Asp Leu Val Ile Lys Tyr Gly Ala Val Asp Pro
165    170    175
Leu Leu Ala Leu Leu Ala Val Pro Asp Met Ser Ser Leu Ala Cys Gly
180    185    190
Tyr Leu Arg Asn Leu Thr Trp Thr Leu Ser Asn Leu Cys Arg Asn Lys
195    200    205
Asn Pro Ala Pro Pro Ile Asp Ala Val Glu Gln Ile Leu Pro Thr Leu
210    215    220
Val Arg Leu Leu His His Asp Asp Pro Glu Val Leu Ala Asp Thr Cys
225    230    235    240
Trp Ala Ile Ser Tyr Leu Thr Asp Gly Pro Asn Glu Arg Ile Gly Met
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Val Val Lys Thr Gly Val Val Pro Gln Leu Val Lys Leu Leu Gly Ala
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Ser Glu Leu Pro Ile Val Thr Pro Ala Leu Arg Ala Ile Gly Asn Ile
275    280    285
Val Thr Gly Thr Asp Glu Gln Thr Gln Val Val Ile Asp Ala Gly Ala
290    295    300
Leu Ala Val Phe Pro Ser Leu Leu Thr Asn Pro Lys Thr Asn Ile Gln
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Lys Glu Ala Thr Trp Thr Met Ser Asn Ile Thr Ala Gly Arg Gln Asp
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Met Gly Ser Pro  
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5 10 15 20

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Ile Ile His Arg Val His Leu Arg Gly Ser Phe Gln Val Thr Arg Ala  
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Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly Arg Ile Ile Met Thr  
135 140 145

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Gly	Arg	Lys	Ser	Asn	Ile	His	Cys	Asn	Thr	Ile	Ala	Pro	Asn	Ala	Gly	
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Ser	Arg	Met	Thr	Gln	Thr	Val	Met	Pro	Glu	Asp	Leu	Val	Glu	Ala	Leu	
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Lys	Pro	Glu	Tyr	Val	Ala	Pro	Leu	Val	Leu	Trp	Leu	Cys	His	Glu	Ser	
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Cys	Glu	Glu	Asn	Gly	Gly	Leu	Phe	Glu	Val	Gly	Ala	Gly	Trp	Ile	Gly	
	230					235					240					
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Lys	Leu	Arg	Trp	Glu	Arg	Thr	Leu	Gly	Ala	Ile	Val	Arg	Gln	Lys	Asn	
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cac	cca	atg	act	cct	gag	gca	gtc	aag	gct	aac	tgg	aag	aag	atc	tgt	931
His	Pro	Met	Thr	Pro	Glu	Ala	Val	Lys	Ala	Asn	Trp	Lys	Lys	Ile	Cys	
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Asp	Phe	Glu	Asn	Ala	Ser	Lys	Pro	Gln	Ser	Ile	Gln	Glu	Ser	Thr	Gly	
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Leu	Glu	Ala	Ile	Met	Tyr	Ala	Leu	Gly	Val	Gly	Ala	Ser	Ile	Lys	Asp	
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Pro	Lys	Asp	Leu	Lys	Phe	Ile	Tyr	Glu	Gly	Ser	Ser	Asp	Phe	Ser	Cys	
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Leu	Pro	Thr	Phe	Gly	Val	Ile	Ile	Gly	Gln	Lys	Ser	Met	Met	Gly	Gly	
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gga	tta	gca	gaa	att	cct	gga	ctt	tca	atc	aac	ttt	gca	aag	gtt	ctt	1315
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cat	gga	gag	cag	tac	tta	gag	tta	tat	aaa	cca	ctt	ccc	aga	gca	gga	1363
His	Gly	Glu	Gln	Tyr	Leu	Glu	Leu	Tyr	Lys	Pro	Leu	Pro	Arg	Ala	Gly	

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ggt gta gtg att att atg gat gtc tat tct tat tct gag aag gaa ctt	1459						
Gly Val Val Ile Ile Met Asp Val Tyr Ser Tyr Ser Glu Lys Glu Leu		440		445		450	
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Ile Cys His Asn Gln Phe Ser Leu Phe Leu Val Gly Ser Gly Gly Phe		455		460		465	
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Gly Gly Lys Arg Thr Ser Asp Lys Val Lys Val Ala Val Ala Ile Pro		470		475		480	
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Asn Arg Pro Pro Asp Ala Val Leu Thr Asp Thr Thr Ser Leu Asn Gln		485		490		495	500
gct gct ttg tac cgc ctc agt gga gac cgg aat ccc tta cac att gat	1651						
Ala Ala Leu Tyr Arg Leu Ser Gly Asp Arg Asn Pro Leu His Ile Asp		505		510		515	
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Leu Cys Thr Phe Gly Phe Ser Ala Arg Arg Val Leu Gln Gln Phe Ala		535		540		545	
gat aat gat gtg tca aga ttc aag gca gtt aag gct cgt ttt gca aaa	1795						
Asp Asn Asp Val Ser Arg Phe Lys Ala Val Lys Ala Arg Phe Ala Lys		550		555		560	
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665 670 675

ggc cct gca aaa ggt gct gct gat aca aca atc ata ctt tca gat gaa 2179
Gly Pro Ala Lys Gly Ala Ala Asp Thr Thr Ile Ile Leu Ser Asp Glu
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Asp Phe Met Glu Val Val Leu Gly Lys Leu Asp Pro Gln Lys Ala Phe
695 700 705

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Phe Ser Gly Arg Leu Lys Ala Arg Gly Asn Ile Met Leu Ser Gln Lys
710 715 720

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Leu Gln Met Ile Leu Lys Asp Tyr Ala Lys Leu *
725 730 735

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Gly Gly Lys Ala Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu Lys
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Val Val Lys Thr Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val Val
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Glu Asp Trp Asp Ile Ile His Arg Val His Leu Arg Gly Ser Phe Gln
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Val Thr Arg Ala Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly Arg
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Ile Ile Met Thr Ser Ser Ala Ser Gly Ile Tyr Gly Asn Phe Gly Gln
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Leu Ala Ile Glu Gly Arg Lys Ser Asn Ile His Cys Asn Thr Ile Ala
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Val	Ala	Ile	Pro	Asn	Arg	Pro	Pro	Asp	Ala	Val	Leu	Thr	Asp	Thr	Thr
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Gln	Lys	Ala	Phe	Phe	Ser	Gly	Arg	Leu	Lys	Ala	Arg	Gly	Asn	Ile	Met		
705					710					715					720		
Leu	Ser	Gln	Lys	Leu	Gln	Met	Ile	Leu	Lys	Asp	Tyr	Ala	Lys	Leu			
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